

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/691,532
Source: FPW0
Date Processed by STIC: 10/21/04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/21/2004

PATENT APPLICATION: US/10/691,532

TIME: 10:38:51

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10212004\J691532.raw

```

3 <110> APPLICANT: JOHNSON, BRUCE FLETCHER
4     SYUD, FAISAL
6 <120> TITLE OF INVENTION: LABELED PEPTIDES FOR LECTIN-LIKE OXIDIZED LOW-DENSITY
7     LIPOPROTEIN RECEPTOR (LOX-1)
9 <130> FILE REFERENCE: 130984-1
11 <140> CURRENT APPLICATION NUMBER: 10/691,532
12 <141> CURRENT FILING DATE: 2003-10-24
14 <160> NUMBER OF SEQ ID NOS: 11
16 <170> SOFTWARE: PatentIn Ver. 3.2
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 5
20 <212> TYPE: PRT
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
25     peptide
27 <220> FEATURE:
28 <221> NAME/KEY: MOD_RES
29 <222> LOCATION: (3)
30 <223> OTHER INFORMATION: Ile or Arg
32 <400> SEQUENCE: 1
W--> 33 Leu Ser Xaa Pro Pro
34     1             5
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 6
39 <212> TYPE: PRT
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
44     peptide
46 <220> FEATURE:
47 <221> NAME/KEY: MOD_RES
48 <222> LOCATION: (5)
49 <223> OTHER INFORMATION: Thr or Arg
51 <400> SEQUENCE: 2
W--> 52 Leu Thr Pro Ala Xaa Ala
53     1             5
56 <210> SEQ ID NO: 3
57 <211> LENGTH: 7
58 <212> TYPE: PRT
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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63      peptide
65 <400> SEQUENCE: 3
66 Met Thr Thr Pro Pro Leu Thr
67 1 5
70 <210> SEQ ID NO: 4
71 <211> LENGTH: 5
72 <212> TYPE: PRT
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
77      peptide
79 <220> FEATURE:
80 <221> NAME/KEY: MOD_RES
81 <222> LOCATION: (5)
82 <223> OTHER INFORMATION: Tyr or Leu
84 <400> SEQUENCE: 4
W--> 85 Leu Thr Arg Pro Xaa
86 1 5
89 <210> SEQ ID NO: 5
90 <211> LENGTH: 6
91 <212> TYPE: PRT
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
96      peptide
98 <220> FEATURE:
99 <221> NAME/KEY: MOD_RES
100 <222> LOCATION: (4)
101 <223> OTHER INFORMATION: Pro or Arg
103 <400> SEQUENCE: 5
W--> 104 Met Thr Ala Xaa Pro Ile
105 1 5
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 4
110 <212> TYPE: PRT
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
115      peptide
117 <400> SEQUENCE: 6
118 Lys Lys Gly Gly
119 1
122 <210> SEQ ID NO: 7
123 <211> LENGTH: 11
124 <212> TYPE: PRT
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
129      peptide

```

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131 <400> SEQUENCE: 7
132 Lys Lys Gly Gly Phe Gln Thr Pro Pro Gln Leu
133   1           5           10
136 <210> SEQ ID NO: 8
137 <211> LENGTH: 10
138 <212> TYPE: PRT
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
143     peptide
145 <400> SEQUENCE: 8
146 Arg Gly Ala Val Tyr Ala Glu Asn Cys Ile
147   1           5           10
150 <210> SEQ ID NO: 9
151 <211> LENGTH: 11
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
157     peptide
159 <400> SEQUENCE: 9
160 Lys Gly Lys Gly Gln Pro Leu Phe Thr Pro Gln
161   1           5           10
164 <210> SEQ ID NO: 10
165 <211> LENGTH: 1318
166 <212> TYPE: DNA
167 <213> ORGANISM: Homo sapiens
169 <220> FEATURE:
170 <221> NAME/KEY: CDS
171 <222> LOCATION: (127)..(945)
173 <400> SEQUENCE: 10
174 ggggccgcac tagtgattct gggtcggccc acctctgaag gttccagaat cgatagtga 60
176 ttcgtgattt tagttgttg aagttcgtga ctgcttcact ctctcattct tagcttgaat 120
178 ttggaa atg act ttt gat gac cta aag atc cag act gtg aag gac cag 168
179     Met Thr Phe Asp Asp Leu Lys Ile Gln Thr Val Lys Asp Gln
180       1           5           10
182 cct gat gag aag tca aat gga aaa aaa gct aaa ggt ctt cag ttt ctt 216
183 Pro Asp Glu Lys Ser Asn Gly Lys Lys Ala Lys Gly Leu Gln Phe Leu
184 15           20           25           30
186 tac tct cca tgg tgg tgc ctg gct gct gcg act cta ggg gtc ctt tgc 264
187 Tyr Ser Pro Trp Trp Cys Leu Ala Ala Ala Thr Leu Gly Val Leu Cys
188           35           40           45
190 ctg gga tta gta gtg acc att atg gtg ctg ggc atg caa tta tcc cag 312
191 Leu Gly Leu Val Val Thr Ile Met Val Leu Gly Met Gln Leu Ser Gln
192           50           55           60
194 gtg tct gac ctc cta aca caa gag caa gca aac cta act cac cag aaa 360
195 Val Ser Asp Leu Leu Thr Gln Glu Gln Ala Asn Leu Thr His Gln Lys
196           65           70           75
198 aag aaa ctg gag gga cag atc tca gcc cgg caa caa gca gaa gaa gct 408

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```

199 Lys Lys Leu Glu Gly Gln Ile Ser Ala Arg Gln Gln Ala Glu Glu Ala
200      80                      85                      90
202 tca cag gag tca gaa aac gaa ctc aag gaa atg ata gaa acc ctt gct 456
203 Ser Gln Glu Ser Glu Asn Glu Leu Lys Glu Met Ile Glu Thr Leu Ala
204 95                      100                      105                      110
206 cgg aag ctg aat gag aaa tcc aaa gag caa atg gaa ctt cac cac cag 504
207 Arg Lys Leu Asn Glu Lys Ser Lys Glu Gln Met Glu Leu His His Gln
208                      115                      120                      125
210 aat ctg aat ctc caa gaa aca ctg aag aga gta gca aat tgt tca gct 552
211 Asn Leu Asn Leu Gln Glu Thr Leu Lys Arg Val Ala Asn Cys Ser Ala
212                      130                      135                      140
214 cct tgt ccg caa gac tgg atc tgg cat gga gaa aac tgt tac cta ttt 600
215 Pro Cys Pro Gln Asp Trp Ile Trp His Gly Glu Asn Cys Tyr Leu Phe
216                      145                      150                      155
218 tcc tcg ggc tca ttt aac tgg gaa aag agc caa gag aag tgc ttg tct 648
219 Ser Ser Gly Ser Phe Asn Trp Glu Lys Ser Gln Glu Lys Cys Leu Ser
220                      160                      165                      170
222 ttg gat gcc aag ttg ctg aaa att aat agc aca gct gat ctg gac ttc 696
223 Leu Asp Ala Lys Leu Leu Lys Ile Asn Ser Thr Ala Asp Leu Asp Phe
224 175                      180                      185                      190
226 atc cag caa gca att tcc tat tcc agt ttt cca ttc tgg atg ggg ctg 744
227 Ile Gln Gln Ala Ile Ser Tyr Ser Ser Phe Pro Phe Trp Met Gly Leu
228                      195                      200                      205
230 tct cgg agg aac ccc agc tac cca tgg ctc tgg gag gac ggt tct cct 792
231 Ser Arg Arg Asn Pro Ser Tyr Pro Trp Leu Trp Glu Asp Gly Ser Pro
232                      210                      215                      220
234 ttg atg ccc cac tta ttt aga gtc cga ggc gct gtc tcc cag aca tac 840
235 Leu Met Pro His Leu Phe Arg Val Arg Gly Ala Val Ser Gln Thr Tyr
236                      225                      230                      235
238 cct tca ggt acc tgt gca tat ata caa cga gga gct gtt tat gcg gaa 888
239 Pro Ser Gly Thr Cys Ala Tyr Ile Gln Arg Gly Ala Val Tyr Ala Glu
240                      240                      245                      250
242 aac tgc att tta gct gcc ttc agt ata tgt cag aag aag gca aac cta 936
243 Asn Cys Ile Leu Ala Ala Phe Ser Ile Cys Gln Lys Lys Ala Asn Leu
244 255                      260                      265                      270
246 aga gca cag tgaatttgaa ggctctggaa gaaaagaaaa aagtctttga 985
247 Arg Ala Gln
249 gttttattct ggaatttaag ctattctttg tcacttgggt gccaaacatg agagcccaga 1045
251 aaactgtcat ttagctggct gcagaactcc tttgcagaaa ctgggggtcc aggtgcctgg 1105
253 cacctttatg tcaacatttt tgattctagc tatctgtatt atttcacctt gcttgtccca 1165
255 agcttccctg ccagcctgaa gtccattttc ccctttttat tttaaaattt gactcctctt 1225
257 caagcttgaa aaccctctga actcagtctt ctttacctca ttatcacctt cccctcacac 1285
259 tcctaaaatt gcatgaaaga cagaccggaa ttc 1318
262 <210> SEQ ID NO: 11
263 <211> LENGTH: 273
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens.
267 <400> SEQUENCE: 11
268 Met Thr Phe Asp Asp Leu Lys Ile Gln Thr Val Lys Asp Gln Pro Asp

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```

269      1              5              10              15
271 Glu Lys Ser Asn Gly Lys Lys Ala Lys Gly Leu Gln Phe Leu Tyr Ser
272              20              25              30
274 Pro Trp Trp Cys Leu Ala Ala Ala Thr Leu Gly Val Leu Cys Leu Gly
275              35              40              45
277 Leu Val Val Thr Ile Met Val Leu Gly Met Gln Leu Ser Gln Val Ser
278              50              55              60
280 Asp Leu Leu Thr Gln Glu Gln Ala Asn Leu Thr His Gln Lys Lys Lys
281 65              70              75              80
283 Leu Glu Gly Gln Ile Ser Ala Arg Gln Gln Ala Glu Glu Ala Ser Gln
284              85              90              95
286 Glu Ser Glu Asn Glu Leu Lys Glu Met Ile Glu Thr Leu Ala Arg Lys
287              100              105              110
289 Leu Asn Glu Lys Ser Lys Glu Gln Met Glu Leu His His Gln Asn Leu
290              115              120              125
292 Asn Leu Gln Glu Thr Leu Lys Arg Val Ala Asn Cys Ser Ala Pro Cys
293 130              135              140
295 Pro Gln Asp Trp Ile Trp His Gly Glu Asn Cys Tyr Leu Phe Ser Ser
296 145              150              155              160
298 Gly Ser Phe Asn Trp Glu Lys Ser Gln Glu Lys Cys Leu Ser Leu Asp
299              165              170              175
301 Ala Lys Leu Leu Lys Ile Asn Ser Thr Ala Asp Leu Asp Phe Ile Gln
302              180              185              190
304 Gln Ala Ile Ser Tyr Ser Ser Phe Pro Phe Trp Met Gly Leu Ser Arg
305              195              200              205
307 Arg Asn Pro Ser Tyr Pro Trp Leu Trp Glu Asp Gly Ser Pro Leu Met
308 210              215              220
310 Pro His Leu Phe Arg Val Arg Gly Ala Val Ser Gln Thr Tyr Pro Ser
311 225              230              235              240
313 Gly Thr Cys Ala Tyr Ile Gln Arg Gly Ala Val Tyr Ala Glu Asn Cys
314              245              250              255
316 Ile Leu Ala Ala Phe Ser Ile Cys Gln Lys Lys Ala Asn Leu Arg Ala
317              260              265              270
319 Gln

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 3
Seq#:2; Xaa Pos. 5
Seq#:4; Xaa Pos. 5
Seq#:5; Xaa Pos. 4

VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

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L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0

L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0

L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0